Effect of Taxonomic Resolution on Detection of Benthic Impacts of Salmon Farming in British Columbia

James E. Dalby Jr., J. Bernie Taekema, *and* ***Eric R. McGreer***
British Columbia Ministry of Water, Land, & Air Protection, Nanaimo, BC

Abstract
Studies of the effects of human disturbances on marine benthic communities often include taxonomic analysis of invertebrates. Unfortunately, identification to the taxonomic level of species tends to be time-consuming and expensive. If detection of impacts were as likely using data at taxonomically higher levels (genus, family, order, class, phylum), then we could justify identifying the biota to these levels instead, and potentially save much time and money. Family is the ideal level for 3 Mediterranean communities impacted by aquaculture, but not necessarily for other communities (Karakassis & Hatziyanni 2000). In 2000, we collected biological sediment samples near fish farms on the British Columbia coast. Univariate statistical analyses (ANOVA, regression) applied to taxon richness data show that impacts are detectable at taxonomic levels no higher than family or order, depending on distance from farm, farm site, and statistical test used. Results of multivariate analyses (MDS, ANOSIM) will also be presented. These early findings suggest that it would be reasonable to identify invertebrates to levels above species in future BC aquaculture studies. Researchers studying other kinds of human disturbances in the GB/PS region may be able to reduce costs and time spent obtaining invertebrate data by doing analyses of this kind.

Extended Abstract
Many marine benthic monitoring studies involve taxonomic identification of invertebrates to the species level. Unfortunately, this work is time-consuming and expensive because of its painstaking nature, and the shortage of taxonomists. Much effort could be saved, and turnaround times reduced, if identifying the fauna to higher taxonomic levels, such as genus or family, would enable detection of impacts.

The new BC *Finfish Aquaculture Waste Control Regulation (FAWCR)*, enacted on 12 September 2002, requires soft bottom invertebrates collected during operational monitoring to be taxonomically identified to the level of family. The basis of this requirement was scientific literature, e.g. Karakassis & Hatziyanni (2000) reported that family level was sufficient for detecting benthic impacts of aquaculture in the Mediterranean. Other studies of marine benthos done in other parts of Europe, California, and Antarctica, have likewise shown that taxonomic identification above species is sufficient for detecting other kinds of human disturbances. We are unaware of any published studies of this kind for marine benthos in the Pacific Northwest.

Over the past 3 years, we have sampled sediments at nearly half of the ≈ 120 finfish farms on the BC coast, obtaining biological data from many of them. We recently used data collected at Power Bay on 26 September 2000, to help determine what taxonomic level would be appropriate for anticipated amendments to the *FAWCR* in 2007. We chose this farm site for our analysis because, unlike all others visited, it lies within the Georgia Basin. Based on previous exploratory data analyses (Erickson et al. 2001), our impression was that this farm has had a medium level impact on the benthos.

We collected sediment samples along a single transect at 5, 35, 60, and 100 m from the net pens, and at one reference station located 635 m from the net pens. Three ponar grabs were collected at each distance, except 100 m where only 2 were collected because of a difficult seabed. Sampling depths ranged from 51 to 57 m across all stations, and sediment grain sizes varied from 3 to 22% silt/clay at farm stations, to 63% silt/clay at the reference station.

When the data for all sampling stations were pooled, there were 202 species within 161 genera, within 92 families, within 50 orders, within 22 classes, within 10 phyla. There were 3 major phyla, the most species being Annelida (almost entirely polychaetes), followed by Arthropoda (almost entirely crustaceans), then Mollusca (mainly snails and clams). Finally, there were several minor phyla (e.g. Sipuncula, Echinodermata).

For the univariate statistical analyses, stations were compared in terms of species richness using 1-way Analysis of Variance, followed by Student Newman Keuls tests. Where necessary, the data were log-transformed before analysis. The tests showed that the number of species increased significantly with distance from the farm. Thus, there was no difficulty detecting the pollution gradient at species level.

The same conclusion was reached for data aggregated to the level of genus: significantly more genera were encountered at stations located further from the farm. The conclusion was the same for family level, although there were only 2 significant pairwise differences, as compared to 6 significant pairwise differences for both species and genus levels. At the level of order, differences among stations were only marginally significant. At class level, no significant differences were detected, and there was even less evidence for any differences at phylum level.

For the multivariate analyses, after being log-transformed to increase the importance of rare species, the data were analyzed by Multi-dimensional Scaling to enable differences in species composition among stations to be visualized in ordinations. Then one-way Analysis of Similarity tests were used to test for differences in species compositions among stations. Using these procedures, there was clear evidence for a pollution gradient at species level.

When applied to genus and family level data, the statistics again revealed the pollution gradient. At order level, the gradient was less clear in the ordination, but the statistical test was still significant. There was more deterioration of the visual pattern at class level, but significant differences were again detected. Finally, we noted significant differences at phylum level, but the gradient was less apparent than before.

In summary, the statistical analyses were able to detect biological impacts at taxonomic levels as high as family (univariate analyses) and phylum (multivariate). These findings suggest that there is justification to require family or higher taxonomic levels in the next version of the regulation. Furthermore, our decision to require family level in the present regulation appears to have been appropriate. That our results are consistent with the findings of other researchers in different parts of the world adds to the credibility of our results.

However, we stress that this research is not yet complete. More analyses must be done to answer questions like:

- Does the appropriate taxonomic level depend on environment (e.g. geographic region, bottom type)?
- Does it depend on type of study design (gradient vs. control-impact designs, sample sizes)?
- Does it depend on level of pollution (high, medium, low)?
- Would exclusion of minor phyla (e.g. Sipuncula) make much of a difference?
- Would inclusion of only one major taxon (e.g. Polychaeta) suffice?

We will be able to decide upon the best taxonomic level for the next version of the regulation only after this additional information has been gathered. In the meantime, we urge researchers studying human disturbances of marine benthos in the Georgia Basin/Puget Sound region to consider identifying the fauna to family level or higher, to save time and money spent on taxonomic analyses.

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